

THE I.M.A.G.E. CONSORTIUM: Future Directions
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The I.M.A.G.E. Consortium was founded in 1993 to accelerate gene discovery through the use of arrayed gene libraries, and to aid in the accumulation of sequence, map, and expression information for all genes through an Integrated Molecular Analysis of Genomes and their Expression. The human genome is the first to be studied, with over 250,000 arrayed human clones from 25 different cDNA libraries now available through a network of five distributors. Primarily through the efforts of the WashU-Merck Gene Index collaborators, over 280,000 EST sequences derived from these clones have been deposited in dbEST. The estimate of the number of distinct 3' ends (and thus an approximation of the number of distinct genes) is currently around 40,000.

Directionally cloned, oligo (dT)-primed plasmid cDNA libraries are obtained from several commercial and private sources, with the bulk of the clones derived from normalized libraries made by Dr. M. Bento Soares (Columbia Univ). Clones are arrayed at Lawrence Livermore National Laboratory, assigned unique I.M.A.G.E. CloneIDs, and sent to Washington University for sequencing, sizing, and analysis. All suitable sequences are annotated and deposited immediately into the NCBI dbEST database. At this time, mapping data is available through the Whitehead Institute at MIT and the Stanford Human Genome Center. Over 1,000 laboratories worldwide have already received the (royalty-free) I.M.A.G.E. Consortium clones and have agreed to submit additional sequence, mapping, and expression data to public databases.

We will report on the current status of this work, along with the progress being made on three fronts: (i) the expansion of the Consortium collection to include mouse cDNA clones, (ii) efforts to maximize the efficiency of finding the remaining as-yet-undiscovered genes, and (iii) improved WWW-based access to integrated views of sequence, map, and expression information for each clone. Further information about the I.M.A.G.E. Consortium is available by email (info@image.llnl.gov) or through the WWW (<http://www-bio.llnl.gov/bbrp/image/image.html>).

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